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/clone="RPCI-24-294M13"

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/clone.lib="RBCI-24"/sex="Male"

/sex="Male"

/cell\_type="Spleen/Bra

/NOTE- VECTOR: PIARBA

RPCI-24 Mouse BAC Library

library was cloned into

BamHI sites using MboI

base pair sites using MBP-DNA.

DNA. 142 = 161 =

a 148 c 164 g

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DATA COLUMNS  
ORIGIN

Search completed: June 12, 2002, 07:56:52  
Job time: 24667 sec

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OM nucleic - nucleic search, using sw model

Run on: June 12, 2002, 01:35:49 ; Search time 2989.43 Seconds  
(without alignments)  
11270 284 Million cell updates/sec

Title: US-09-647-522-4

Perfect score: 1610

Sequence: 1 gcacaaggcactttggtaaq.....aaaaaaacaaaaaaaaaaa 1610

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_stc:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hun:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sis:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htgo\_inv:\*

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2 277 17.2 1602 3 AB036714 AB036714 Carybdea  
3 48.6 3.0 7218 6 AB045319 AB045319 Chirospal  
4 47 1938 6 AX251552 Sequence  
5 46.2 2.9 56153 6 AX251552 Sequence  
6 43.8 2.7 15548 6 AX347057 Sequence  
7 43.2 2.7 9733 6 AX345584 Sequence  
8 42.8 2.7 1141 6 AX083744 Sequence  
9 42.8 2.7 1240 3 AF104650 AF104650 lasioglos  
10 42.8 2.7 7001 6 AX347354 Sequence  
11 42.8 2.7 7001 6 AX349075 Sequence  
12 42.8 2.7 7302 6 AX345613 Sequence  
13 42.8 2.7 174019 9 AP001538 Homo sapi  
14 42.8 2.7 340000 9 AP001674 Homo sapi  
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16 42.2 2.6 98975 9 AC004975 Homo sapi  
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19 41.8 2.6 200317 9 HS69B13 Human DNA  
20 41.8 2.6 254534 2 AC097326 Pan trogl  
21 41.6 2.6 140934 9 AC009491 Homo sapi  
22 41.6 2.6 169728 2 AC026183 Homo sapi  
23 41.4 2.6 349980 6 AX344565 Sequence  
24 41.2 2.6 38342 6 AX251504 Sequence  
25 41.2 2.6 38342 6 AX344503 Sequence  
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28 40.6 2.5 5216 6 AX281348 Sequence  
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30 40.6 2.5 7113 6 AX345707 Sequence  
31 40.6 2.5 183272 2 AC094428 Rattus no  
32 40.6 2.5 204429 2 AC005506 Plasmodiu  
33 40.6 2.5 250172 2 AC005139 Plasmodiu  
34 40.6 2.5 310779 2 AC005140 Plasmodiu  
35 40.4 2.5 7037 6 AX346653 Sequence  
36 40.4 2.5 7195 6 AX277866 Sequence  
37 40.4 2.5 7195 6 AX32551 Sequence  
38 40.4 2.5 188660 2 AC068425 Mus muscu  
39 40.4 2.5 188826 9 AL35980 Human DNA  
40 40.2 2.5 3678 1 BC011531 Mus muscu  
41 40.2 2.5 302750 1 AP003133 Staphyloc  
42 40.2 2.5 366900 1 AP003362 U23511 Caenorhabdi  
43 40 2.5 47703 40 U23511 Caenorhabdi  
44 40 2.5 106076 9 AC008465 Homo sapi  
45 40 2.5 152771 9 AP004241 Homo sapi

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ALIGNMENTS

RESULT 1 AB015878

LOCUS AB015878 1630 bp mRNA linear INV 06-SEP-2000

DEFINITION Carybdea rastonii crt-1 mRNA for toxin-1, complete cds.

ACCESSION AB015878

VERSION AB015878.1 GI:9988401

KEYWORDS toxin-1.

SOURCE Carybdea rastonii cDNA to mRNA.

ORGANISM Carybdea rastonii  
Eukaryota; Metazoa; Cnidaria; Cubozoa; Cubomedusae; Carybdeidae;

REFERENCE Nagai,H., Takuwa,K., Nakao,M., Ito,E., Miyake,M., Noda,M. and  
Nakajima,T.

TITLE Novel proteinaceous toxins from the box jellyfish (Sea wasp)

JOURNAL Biochem. Biophys. Res. Commun. 275 (2), 582-588 (2000)

MEDLINE 2042301

REFERENCE 2 (bases 1 to 1630)

AUTHORS Nagai,H. and Takuwa,K.

TITLE Direct Submission

JOURNAL Submitted (29-JUN-1998) Hiroshi Nagai, Suntory Institute for  
Bioorganic Research; Wakayama Dai 1-1-1, Shimamoto, Osaka 618-8503,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Match Length	DB ID	Description



KEYWORDS	toxin-A.
SOURCE	Carybdea alata cDNA to mRNA.
ORGANISM	Carybdea alata
REFERENCE	Eukaryota; Metazoa; Cnidaria; Cubozoa; Cubomedusae; Carybdeidae; Carybdea 1 (sites)
AUTHORS	Nagai,H., Takuwa,K., Nakao,M., Sakamoto,B., Crow,G.L. and Nakajima,T.
TITLE	Isolation and characterization of a novel protein toxin from the hawaiian box jellyfish (Sea wasp) <i>carybdea alata</i> .
JOURNAL	Biochem. Biophys. Res. Commun. 275 (2), 589-594 (2000)
MEDLINE	20422302
REFERENCE	2 (bases 1 to 1602)
AUTHORS	Nagai,H.
TITLE	Direct Submission
JOURNAL	Submitted (07-JAN-2000) Hiroshi Nagai, Suntory Institute for Biorganic Research, 1-1 Wakayamada, Shimamoto, Mishima, Osaka 618-8503, Japan (E-mail:nagai@sunbo.or.jp, Tel:81-75-962-3743, Fax:81-75-962-2115)
FEATURES	Location/Qualifiers
source	1..1602
sig-peptide	/organism="carybdea alata" (ab_xref="taxon:112899" 73..126 /gene="cat-1" /protein_id="BABJ27.1" /db_xref="GI:9988404"
gene	/translation="MERGYSUHLVLFVLSTAFPSOARLRYRRSADAVSTDIDGII GOLDLGDTKRLKEALQGVOBKAEPATKAVTIVSVGGVSISKFSGDPEVA QELEDNYKGAKRTNAVTFNSVSKTELVHDSVRDAVRDAFTNMGVLESRI NRGSVSDNNEAMRTINFLXLOQSMRSLTSPDHSOKTQIYLWKRAGGYDEAISLTS DONKEATRTVFLHOMETKYLQFQGKQYVDPYHDPARPTED GLYYRMONRANNRISCKSTAGNHRNGKCDSSKGIRKLKENHTLTLSRAM VIRKAQJWGWGJADEDPGEQSYTFPLTINGFYMVKWPDYFVYMESSAHGYIRSW HYNPDRQGQWKIL"
BASE COUNT	467 a 324 c 356 g 455 t
ORIGIN	
Query Match	17.2%; Score 277; DB 3; Length 1602;
Best Local Similarity	54.1%; Pred. No. 1.8e-55;
Matches	634; Conservative 0; Mismatches 525; Indels 12; Gaps 3;
Qy	221 ttgacaaggcacaaaatcttctggactgtcgatcgcttttagaaattaattctg 299 trccTAAGTCACATCAGGGCTCTGGAGTCATGAGCAAGTCAAGTCAGTCAG
Db	281 gagatgcaccaaatatttttgtggatccccgacattgttgccagaatttcaactt 359 GAGATCCCTTGATGTGCTCAGGGCTCTGGAGTCATGAGCAAGTCAAGTCAG
Qy	341 ttggaggcccttcggatggaaatcgagcgatgttttttttttttttttttttttttt 419 TGGAGGHRCCAPCGGGATTCTATGGGCACTGATCATCTGATTCCTCTCTTA
Db	401 cttgttttacttgcgaacctgcacaaaggaaacttgcgttttttttttttttttttttt 479 GCCTCTCTCGCAATAGTATGGAACTGCATCACAGTTGACCAAGCTTC
Qy	461 gcaagcatcgatcgatggccatccaagacttgcaggggccaggatgttttttttttt 539 AGAAATATCGGCACTCAAGAGTGGAGACAATGTAAGAGCAAAGGACTTAAATG
Db	521 atcatatgtgttt 599 CGGTCACTCACCTCGTCAACAGTGTATCAAAGACAGAGARTGACCGAGGTCATTG
RESULT	3
LOCUS	166494_c
DEFINITION	Sequence 14 from patent US 5670367.
ACCESSION	166494
VERSION	166494.1 GI:2724471
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 7218)
AUTHORS	Dorner,F., Scheiflinger,F. and Falkner,F. Gunter.
JOURNAL	Recombinant fowlpox virus
FEATURES	Patent: US 5670367-A 14 23 -SEP-1997; Location/Qualifiers



Query Match	2.9%	Score 46.2;	DB 6;	Length 56153;					
Best Local Similarity	52.2%	Pred. No. 1.1;	Length 56153;	Matches 128; Conservative 0; Mismatches 113; Indels 4; Gaps 1;					
DEFINITION	Sequence 655 from Patent WO0200928.	ACCESSION	AX345584	VERSION AX345584.1 GI:18493470					
KEYWORDS	synthetic construct.	SOURCE	synthetic construct.	ORGANISM artificial sequence.					
REFERENCE	1 ( <i>sites</i> )	AUTHORS	Olek,A., Piepenbrock,C. and Berlin,K.	TITLE diagnosis of diseases associated with the immune system					
FEATURES	source	JOURNAL	Patent: WO 0200928-A 655 03-JAN-2002; Epigenomics AG (DE)						
BASE COUNT	2955 a 93 c 1898 g 4787 t	ORIGIN	/note="chemically treated genomic DNA (Homo sapiens)" /db_xref="taxon:32630"						
RESULT	6	RESULT	7	RESULT	7				
LOCUS	AX347057	LOCUS	AX345584/C	LOCUS	AX345584				
DEFINITION	Sequence 2128 from Patent WO200928.	DEFINITION	Sequence 655 from Patent WO0200928.	DEFINITION	Sequence 9733 bp DNA				
VERSION	AX347057	ACCESSION	AX345584	ACCESSION	AX345584				
KEYWORDS		VERSION	AX345584.1 GI:18493470	VERSION	PAT 01-FEB-2002				
SOURCE	synthetic construct.	KEYWORDS		KEYWORDS					
ORGANISM	artificial sequence.	SOURCE	synthetic construct.	ORGANISM	synthetic construct.				
REFERENCE	1 ( <i>sites</i> )	AUTHORS	Olek,A., Piepenbrock,C. and Berlin,K.	TITLE	diagnosis of diseases associated with the immune system				
AUTHORS	Olek,A., Piepenbrock,C. and Berlin,K.	JOURNAL	Patent: WO 0200928-A 655 03-JAN-2002; Epigenomics AG (DE)	JOURNAL	Patent: WO 0200928-A 655 03-JAN-2002; Epigenomics AG (DE)				
FEATURES	source	FEATURES	source	FEATURES	source				
SOURCE	1. .15548. /organism="synthetic construct" /db_xref="taxon:32630"	SOURCE	1. .9733. /location/qualifiers 1. .9733. /organism="synthetic construct" /db_xref="taxon:32630"	SOURCE	1. .9733. /location/qualifiers 1. .9733. /organism="synthetic construct" /db_xref="taxon:32630"				
BASE COUNT	4209 a 247 c 2903 g 8189 t	BASE COUNT	2955 a 93 c 1898 g 4787 t	BASE COUNT	2955 a 93 c 1898 g 4787 t				
ORIGIN		ORIGIN		ORIGIN					
RESULT	6	RESULT	7	RESULT	8				
Query Match	2.7%	Score 43.2;	DB 6;	Length 9733;	Query Match	2.7%	Score 43.2;	DB 6;	Length 9733;
Best Local Similarity	51.7%	Pred. No. 6.7;	Length 9733;	Matches 123; Conservative 0; Mismatches 113; Indels 2; Gaps 1;	Best Local Similarity	51.7%	Pred. No. 6.7;	Length 9733;	Matches 123; Conservative 0; Mismatches 113; Indels 2; Gaps 1;
DEFINITION	Sequence 22 from Patent WO0111051.	ACCESSION	AX083744	VERSION AX083744.1 GI:13185472	DEFINITION	Sequence 22 from Patent WO0111051.	ACCESSION	AX083744	VERSION AX083744.1 GI:13185472
VERSION	AX083744.1 GI:13185472	KEYWORDS	synthetic construct.	KEYWORDS	synthetic construct.				
KEYWORDS	synthetic construct.	SOURCE	synthetic construct.	ORGANISM	synthetic construct.				
SOURCE	synthetic construct.	ORGANISM	synthetic construct.	REFERENCE	1 (bases 1 to 1141)				
ORGANISM	artificial sequence.	REFERENCE	1 (bases 1 to 1141)	AUTHORS	Kunst,L. and Clements,S.				
REFERENCE	1 (bases 1 to 1141)	AUTHORS	Kunst,L. and Clements,S.	TITLE	Regulation of embryonic transcription in plants				
AUTHORS	Kunst,L. and Clements,S.	JOURNAL	Patent: WO 011061-A 22 15-FEB-2001; UNIVERSITY OF BRITISH COLUMBIA (CA)	JOURNAL	Patent: WO 011061-A 22 15-FEB-2001; UNIVERSITY OF BRITISH COLUMBIA (CA)				
JOURNAL	UNIVERSITY OF BRITISH COLUMBIA (CA)	FEATURES	source	FEATURES	source				
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BASE COUNT	123 a 32 c 42 g 112 t 832 others	BASE COUNT	123 a 32 c 42 g 112 t 832 others	BASE COUNT	123 a 32 c 42 g 112 t 832 others				
ORIGIN		ORIGIN		ORIGIN					
Query Match	2.7%	Score 42.8;	DB 6;	Length 1141;	Query Match	2.7%	Score 42.8;	DB 6;	Length 1141;



RESULT	10
LOCUS	AX347354
DEFINITION	Sequence 1 from Patent WO200705.
ACCESSION	AX347354
VERSION	AX347354.1 GI:18495242
REFERENCE	Olek,A., Piepenbrock,C. and Berlin,K.
AUTHORS	Method and nucleic acids for the differentiation of astrocytoma, oligoastrocytoma and oligodendroglioma tumor cells
TITLE	Patent: WO 0200705-A 1 03-JAN-2002; Epigenomics AG (DE)
JOURNAL	/db,xref="taxon:32630"/note="Chemically treated genomic DNA (Homo sapiens)"
FEATURES	Location/Qualifiers
SOURCE	1. .7001 /organism="synthetic construct" /db,xref="taxon:32630"
BASE COUNT	2309 a 40 c 1249 g 3403 t
ORIGIN	
Query Match	2.7%; Score 42.8; DB 6; Length 7001;
Best Local Similarity	47.4%; Pred. No. 8.6;
Matches	128; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
QY	1340 aaaaataatccaggaccctcaaggacattggagataacataattaaaggaaatcaaat 1399
Db	3111 AAAATATAATAAACCTAAACAAAATACGTATAATCCCTAAACAAACTAACAC 3052
QY	1400 gtcccaaaggcatacgataataaagacatcaaacgatgcqacttaaqgcacattg 1459
Db	3051 AACTATTTTCTCAATAATAATTTCATTATTATTATTCTATTAT 2992
QY	1460 tatttcacataggatgtcgcatggaaatccataaacccacccggactaattcata 1519
Db	2391 AACTATTTAACAATCATTAATTAATAATTATAATTAACTTCACATCATAAA 2932
QY	1520 ttaaacatataatgtttcttataatgcatttcatgaatctctatgtjacattcag 1579
Db	2931 AAAACTTAATCTTTCTCATTTTACATTAATAATACATATAATATTAATRAAA 2872
QY	1580 agatattgttgtaaaaaaacaaaaaaa 1609
Db	2871 CTAAATAATAATTCCCATAAAATAA 2842
RESULT	12
LOCUS	AX345613
DEFINITION	Sequence 684 from Patent WO200928.
ACCESSION	AX345613
VERSION	AX345613.1 GI:18493499
KEYWORDS	
ORGANISM	synthetic construct
REFERENCE	Olek,A., Piepenbrock,C. and Berlin,K.
AUTHORS	Diagnosis of diseases associated with the immune system
TITLE	Patent: WO 0200928-A 684 03-JAN-2002; Epigenomics AG (DE)
JOURNAL	/db,xref="taxon:32630"/note="Chemically treated genomic DNA (Homo sapiens)"
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Best Local Similarity	47.4%; Pred. No. 8.6;
Matches	128; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
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Db	6955 AAAAACCCATAAAACTATAATAATAATAATAATAATAATAACCTAAACAAAAA 6896
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QY	1460 tatttcacataggatgtcgcatggaaatccataaacccacccggactaattcata 1519
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Db	6775 ATATATTCATACTCTATAATAACATACATAATAACTACGATAATAATTAT 6713
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LOCUS	AX349075
DEFINITION	Sequence 1 from Patent WO200808.
ACCESSION	AX349075
VERSION	AX349075.1 GI:18615110
KEYWORDS	
SOURCE	
ORGANISM	synthetic construct
REFERENCE	(sites) artificial sequence.
AUTHORS	Olek,A., Piepenbrock,C. and Berlin,K.
TITLE	Method and nucleic acids for the analysis of astrocytomas
JOURNAL	Patent: WO 02008-A 1 10-JAN-2002; Epigenomics AG (DE)
FEATURES	Location/Qualifiers
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Best Local Similarity	47.4%; Pred. No. 8.6;
Matches	128; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
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Db	6895 CTCTCATAAACTATAATAATAATAATAATAATAACCTAACAGATTTC 6836
QY	1460 tatttcacataggatgtcgcatggaaatccataaacccacccggactaattcata 1519
Db	6835 ATTTAAATAATAATACTCGGAAACGATAATAATAATAACATACACATA 6776
QY	1520 ttaaacatataatgtttcttataatgcatttcatgaatctctatgtjacattcag 1579
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RESULT 15  
 AC027059/15  
 Locus AC027059  
 Definition Homo sapiens chromosome 4 clone RP11-599J23 map 4, WORKING DRAFT  
 Accession AC027059  
 Version AC027059\_2 GI:759861  
 Keywords HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 Source human.  
 Organism Homo sapiens  
 Reference  
 Authors Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 Title Homo sapiens chromosome 4, clone RP11-599J23  
 Unpublished  
 2 (bases 1 to 195721)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Baldwin,J., Barna,N., Baslien,V., Beda,F.,  
 Boguslavskiy,L., Boukhgatler,B., Brown,A., Burkett,G.,  
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 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,  
 Galagan,J., Gardyne,S., Ginde,S., Goyette,M., Graham,L.,  
 Grand-Pierre,N., Grant,G., Higos,R., Heaford,A., Horton,L.,  
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kahn,L., Karatas,A.,  
 Klein,J., LaRocque,K., Lamakrane,R., Landers,T., Lebo茨ky,J.,  
 Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,  
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeers,R.,  
 Medrini,J., Meneus,L., Mihow,T., Miranda,C., Menga,V., Morrow,J.,  
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,  
 Pianka,C., Pollara,V., Raymond,C., Riley,R., Rodo,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thiermann,N., Stojanovici,N., Subramanian,A., Talamas,J.,  
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (26-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Apr 19, 2000 this sequence version replaced g1:7329419.  
 All repeats were identified using RepeatMasker:  
 Smit,A.F.A. & Green, P. (1996-1997)  
<http://www.genome.washington.edu/RM/RepeatMasker.html>  
 Genome Center  
 Center: Whitehead Institute/MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seg.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 Project Information  
 Center project name: L7408  
 Center clone name: 599\_J\_23  
 ..... Summary statistics  
 Sequencing vector: M13; M77815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0\_960731  
 Consensus quality: 184383 bases at least 040  
 Consensus quality: 191056 bases at least 030  
 Insert size: 17000; agarose-fp  
 Insert size: 17000; sum-of-contigs  
 Quality coverage: 4.6 in Q20 bases; agarose-fp  
 Quality coverage: 4.0 in Q20 bases; sum-of-contigs  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 17 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \*  
 \* 1 1652: contig of 1652 bp in length  
 \* 1653 1752: gap of 100 bp  
 \* 1753 1655: contig of 4810 bp in length  
 \* 6563 6662: gap of 100 bp  
 \* 6663 10464: contig of 3802 bp in length  
 \* 10465 10564: gap of 100 bp  
 \* 10565 15408: contig of 4844 bp in length  
 \* 15409 15508: gap of 100 bp  
 \* 15509 21412: contig of 5904 bp in length  
 \* 21413 21512: gap of 100 bp  
 \* 21513 21760: contig of 6097 bp in length  
 \* 27610 27709: gap of 100 bp  
 \* 27710 32894: contig of 5185 bp in length  
 \* 32895 32944: gap of 100 bp  
 \* 32985 37528: contig of 4554 bp in length  
 \* 37529 37628: gap of 100 bp  
 \* 37629 45785: contig of 8157 bp in length  
 \* 45786 45885: gap of 100 bp  
 \* 45886 58042: contig of 1257 bp in length  
 \* 58043 58442: gap of 100 bp  
 \* 58143 73269: contig of 1527 bp in length  
 \* 73270 73369: gap of 100 bp  
 \* 73370 89505: contig of 16137 bp in length  
 \* 89507 89065: gap of 100 bp  
 \* 89607 104119: contig of 14573 bp in length  
 \* 104180 104279: gap of 100 bp  
 \* 104280 122927: contig of 18648 bp in length  
 \* 122928 123027: gap of 100 bp  
 \* 123028 144803: contig of 21776 bp in length  
 \* 144804 144903: gap of 100 bp  
 \* 144904 1469867: contig of 24964 bp in length  
 \* 169888 169967: gap of 100 bp  
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Search completed: June 12, 2002, 18:00:40  
Job time: 59091 sec

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OM nucleic - nucleic search, using sw model

Run on: June 12, 2002, 02:32:43 ; Search time 278.84 Seconds  
                   (without alignments)

                  9913.328 Million cell updates/sec

Title: US-09-647-522-4

Perfect score: 1610

Sequence: 1 gcacaaagcgacttggtaag . . . . . gaaaagaacaaaaaaaaaa 1610

Scoring table: IDENTITY\_NUC

Searched: Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	1610	100.0	1610 20 AAZZ3610	C. rastonii hemolytic C. alata hemolytic
2	277	2042 22 AAI66621		Tumour suppressor
C	46.2	2.9 56153 22 AAS46794		Human immune system
C	3	43.8 15548 24 ABL34155		Immune system
C	5	43.2 2.7 9733 24 ABL32682		Human immune system
C	6	42.8 2.7 7302 24 ABL32711		Tumour suppressor
C	7	41.2 2.6 38342 22 AAS46746		Sybyean 515002 reg
C	8	41.2 2.6 127197 22 AA161370		Human immune system
C	9	40.6 2.5 5216 24 ABL32347		

## SUMMARIES

FT	PN	W09950294-A1
XX	XX	07-OCT-1999.
PD	XX	30-MAR-1999; 99WO-JP01607.
PF	XX	01-APR-1998; 98JP-0088569.
PR	XX	(SUNR ) SUNTORY LTD.
PA	XX	
PI	XX	Nagai H, Nakajima T;

Human metastasis a Human immune system  
                   Human immune system  
                   Chemically pretrea Nucleic acid sequre  
                   Human gene regulat Human immune syste  
                   Staphylococcus aur Human immune syste  
                   Group B Streptocc Tumour suppressor  
                   Human immune syste Human immune syste  
                   Human diagnostic a Human immune syste  
                   Tumour suppressor Human immune syste  
                   Human immune syste Soybean 318013 reg Drosophila melanog  
                   Human immune syste Human immune syste  
                   Human immune syste Human immune syste  
                   Human metastasis a Human immune syste  
                   Human immune/metasta Human immune/haeema  
                   Human immune/haeema Human immune/haeema  
                   Human immune syste Human immune syste  
                   Human gene regulat Human gene regulat  
                   Enterococcus faecia Human immune/haema Peppermint plant o  
                   Human ORF X ORF1568 Human ORF X ORF1568  
                   Alcohol oxidase ge Staphylococcus aur  
                   Human secreted pro DNA encoding G pro DNA encoding G pro  
                   Drosophila melanog





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PR	01-SEP-2000;	2000DE-1043826.	XX	
PA			AC	ABL3155;
XX			XX	
(EPIG-)	EPIGENOMICS AG.		DT	26-MAR-2002 (first entry)
XX	Olek A., Piepenbrock C., Berlin K;		XX	
DR			DE	Human immune system associated gene SEQ ID NO: 2128.
XX			XX	KW Human; immune system disease; cytosine methylation; antiasthmatic;
PT	Fragments of chemically modified genes associated with tumour suppressor		XX	KW antiarteriosclerotic; antianemic; cytostatic; nonotropic;
PT	genes and oncogenes, useful in designing primers and probes for		XX	KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
PT	analysing diseases associated with cytosine methylation state e.g.		XX	KW antirheumatic; antirheritic; antidiabetic; antipsoriatic;
PT	cancer		XX	KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; anaemia;
PS			XX	KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
XX	Claim 1; SEQ ID NO 520; 27pp; English.		XX	KW gene; ds.
CC	The invention relates to a nucleic acid comprising a sequence of 18		XX	OS Homo sapiens.
CC	bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with		XX	PN WO20020098-A2.
CC	bisulphite, of genes associated with tumour suppression and		XX	XX 03-JAN-2002.
CC	oncogenes having a sequence taken from numbers 408, 458 and 500 are missing from the sequence listing) sequences		XX	XX 02-JUL-2001; 2001WO-EP07537.
CC	{SS} and sequences complementary to {SS}. The nucleic acid may be a		XX	XX 30-JUN-2000; 2000DE-1032529.
CC	peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may		XX	PR 01-SEP-2000; 2000DE-1043826.
CC	form part of a set of probes for detecting the cytosine methylation state		XX	(EPIG-)
CC	and/or single nucleotide polymorphisms and also to be used in an		XX	EPIGENOMICS AG.
CC	array for analysing diseases associated with CpG dinucleotides e.g.		XX	Olek A., Piepenbrock C., Berlin K;
CC	cancers and tumours. The probes can also be used in a method for		XX	DR; 2002-130909/17.
CC	ascertaining genetic and/or epigenetic parameters for the diagnosis		XX	
CC	and/or therapy of existing diseases or the predisposition to specific		XX	Nucleic acid comprising fragment of chemically modified gene, useful
CC	diseases, by analysing cytosine methylations. The parameters may be		XX	for diagnosis and treatment of diseases associated with abnormal
CC	compared to another set of genetic and/or epigenetic parameters, the		XX	cytosine methylation -
CC	differences serving as basis for diagnosis and/or prognosis events which		XX	
CC	are disadvantageous to patients. The present sequence is one of the		XX	
CC	533 genomic sequences derived from tumour suppressor genes and		XX	
CC	oncogenes. Sequences with even numbered Seq ID numbers are the		XX	
CC	complementary sequence of the corresponding odd numbered sequence (e.g.		XX	
CC	ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence		XX	
CC	is missing).		XX	
CC	Note: The sequence data for this Patent did not form part		XX	
CC	of the printed specification, but was obtained in electronic		XX	
CC	format directly from WIPO at		XX	
XX	ftp.wipo.int/pub/published_pct_sequences.		XX	
SQ	Sequence 56153 BP; 15738 A; 1002 C; 12377 G; 27036 T; 0 other;		XX	
Query Match	2 %;	Score 46.2;	DB	22; Length 56153;
Best Local Similarity	52.2 %;	Pred. No.	0.073;	Mismatches 128; Conservative 0; Mismatches 113; Indels 4; Gaps 1;
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Db	11827 AAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 11768			
QY	1460 tattctcacataggatcgctcgatgaatccataacatccggactaaatttcata 1519			
Db	11767 ATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 11708			



CC	differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 553 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence is missing).
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <a href="http://ftpp.wipo.int/pub/published_pct_sequences">ftpp.wipo.int/pub/published_pct_sequences</a> .
CC	Sequence 31342 BP; 12471 A; 472 C; 7153 G; 18246 T; 0 other;
XX	Query Match 2.6%; Score 41.2; DB 22; Length 38342; Best Local Similarity 48.3%; Pad. No. 1; 6; Mismatches 115; Conservative 0; Indels 123; Gaps 0; Matches 115; Mismatches 123; Indels 0; Gaps 0
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Db	17729 AAAATTCATAAAACTTACATATAAACCTAAATTATTTACTA 17670
QY	1432 cgaatcgacttaatgtggacttgcacatcgatgtcgatcaa 1491
Db	17669 TTATACCTTCAAAAAAACTCTCTACTAACTTAATATATAATTAAC 17610
QY	1492 ataaaccatccagcgactaatttccattaaacatataatgtttcttataatgcattt 1551
Db	17609 TAATTTCCCTCCAAAATTCATATACATATAACACTTAAATTAAC 17550
QY	1552 catggatcttcatttgacatttcacagagatgtttttaaagaaaaaaa 1609
Db	17549 ATTATTTATATTCICAAACACTCAAAATACCTTATAATTAAC 17492
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ID	AAS46746/
ID	AAS46746 standard; DNA; 38342 BP.
XX	
AC	AAS46746;
DT	18-DEC-2001 (first entry)
XX	Tumour suppressor gene derived chemically modified sequence #470.
XX	Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CPG dinucleotide; single-nucleotide polymorphism; SNP; tyrosine methylation; ds.
KW	
XX	Homo sapiens.
OS	
XX	W0200168912-A2.
PN	
XX	PD 20-SEP-2001.
XX	PF 15-MAR-2001; 2001WO-EPO2955.
PR	15-MAR-2000; 2000DE-1013847.
PR	05-APR-2000; 2000DE-1019058.
PR	07-APR-2000; 2000DE-1019173.
PR	30-JUN-2000; 2000DE-1032529.
PR	01-SEP-2000; 2000DE-1043826.
XX	PA (EPIG- ) EPIGENOMICS AG.
XX	PT Olek A, Piepenbrock C, Berlin K;
XX	WPI; 2001-602752/68.
XX	Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer
XX	PS Claim 1; SEQ ID NO 470; 27pp; English.
CC	The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically prereated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (SS) and sequences complementary to (SS). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CPG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the
CC	CC differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 553 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence is missing).
CC	CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <a href="http://ftpp.wipo.int/pub/published_pct_sequences">ftpp.wipo.int/pub/published_pct_sequences</a> .
CC	Sequence 31342 BP; 12471 A; 472 C; 7153 G; 18246 T; 0 other;
XX	Query Match 2.6%; Score 41.2; DB 22; Length 38342; Best Local Similarity 48.3%; Pad. No. 1; 6; Mismatches 115; Conservative 0; Indels 123; Gaps 0; Matches 115; Mismatches 123; Indels 0; Gaps 0
QY	1372 ataacctaataaaggaaatcaacatgtcccaaggatcacgatatacgatcaa 1431
Db	17729 AAAATTCATAAACTTACATATAAACCTAAATTATTTACTA 17670
QY	1432 cgaatcgacttaatgtggacttgcacatcgatgtcgatcaa 1491
Db	17669 TTATACCTTCAAAAAAACTCTCTACTAACTTAATATATAATTAAC 17610
QY	1492 ataaaccatccagcgactaatttccattaaacatataatgtttcttataatgcattt 1551
Db	17609 TAATTTCCCTCCAAAATTCATATACATATAACACTTAAATTAAC 17550
QY	1552 catggatcttcatttgacatttcacagagatgtttttaaagaaaaaaa 1609
Db	17549 ATTATTTATATTCICAAACACTCAAAATACCTTATAATTAAC 17492
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ID	AII61370 standard; DNA; 127197 BP.
XX	
AC	AII61370;
XX	
DT	16-OCT-2001 (first entry)
XX	DE Soybean 515002 region G2, SEQ ID NO: 1.
XX	KW Soybean; antihelmintic; gene therapy; soybean cyst nematode; SCN; KW SCN resistance; rhlg; Rhg4; SCN resistant allele; Plant breeding; KW 240017 region G3; 310013 region A3; 515002 region G2; ds.
XX	OS Glycine max.
XX	PT WO200151627-A2.
XX	PD 19-JUL-2001.
XX	PS 05-JAN-2001; 2001WO-US00552.
XX	PR 07-JAN-2000; 2000US-0174880.
XX	DR WPI; 2001-425872/45.
XX	PA (MONS <sup>®</sup> ) MONSANTO CO.
XX	PT New purified nucleic acid for producing a soybean plant having soybean cyst nematode resistance and for use in plant breeding programs - disclosure; Page 131-204; 1353pp; English.
XX	CC The invention relates to nucleic acid molecules from regions of the soybean genome which are associated with soybean cyst nematode (SCN)

CC resistance. The nucleic acids are used to transform plants, and can  
CC produce soybean plants having an Rht4 or an Rht4 SCN resistant allele.  
CC The nucleic acids used for investigating rht4 or Rht4 haplotypes  
CC of soybean plants and for introgressing SCN resistance or partial SCN  
CC resistance into soybean plants. They can also be used in plant breeding  
CC programmes. The invention also relates to proteins encoded by such  
CC nucleic acid molecules, as well as antibodies capable of recognising  
CC these proteins. The present sequence is a nucleic acid molecule  
CC provided in the specification.

xx  
PS Claim 1; SEQ ID NO 320; 32pp + Sequence Listing; German.  
xx  
CC The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
diseases. The present sequence is a gene of the invention.  
xx

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AC		AC		
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KW	Human; immune system disease; cytosine methylation; antiasthmatic;	KW		
KW	antiarteriosclerotic; antiaemic; cytostatic; nootropic;	KW		
KW	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;	KW		
KW	antiinflammatory; antiarthritic; antidiabetic; antipsoriatic;	KW		
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;	KW		
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;	KW		
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XX		OS		
PN	WO200200928-A2.	PN		
XX		PN		
PD	03-JAN-2002.	XX		
XX		PD		
PF	02-JUL-2001; 2001WO-EP07537.	XX		
XX		PF		
PR	30-JUN-2000; 2000DE-103229.	XX		
PR	01-SEP-2000; 2000DE-1043826.	PR	06-APR-2000; 2000DE-1019058.	
XX		PR	07-APR-2000; 2000DE-1019173.	
PA	(EPIG-) EPIGENOMICS AG.	PR	30-JUN-2000; 2000DE-103229.	
XX		PR	01-SEP-2000; 2000DE-1043826.	
PI	Olek A, Piepenbrock C, Berlin K;	XX		
XX		PA	(EPIG-) EPIGENOMICS AG.	
DR	WPI; 2002-130909/17.	XX		
XX		PT	Olek A, Piepenbrock C, Berlin K;	
PT	Nucleic acid comprising fragment of chemically modified gene, useful	XX		
PT	for diagnosis and treatment of diseases associated with abnormal	DR	WPI; 2002-010922/01.	
PT	cytosine methylation -	XX	New nuclear acid derived from chemically treated template -	





PI	Cassel GH, Chen EY, Glass JI, Glass JS, Heiner CR;	XX	06-APR-2001; 2001WO-EP03968.
Lefkowitz E;			
XX			
DR	WPI; 1999-469343/39.	XX	
XX	Detection of ureaplasma urealyticum using novel genes, probes and		
PT	primers	XX	
PS	Claim 1; Page 18-19; 110pp; English.	XX	
XX	The present invention provides methods for the detection and diagnosis	CC	
CC	of ureaplasma urealyticum infection. It provides novel genes	CC	
CC	(AAX9501-601) that can be used as a source of primers and probes for the	CC	
CC	detection of or quantification of U. urealyticum in a biological	CC	
CC	sample. The probes that can be used in the method of the invention by	CC	
CC	forming target:probe complex is complementary to a region selected from	CC	
CC	one of the 181 nucleic acid sequences (AAX9501-681). U. urealyticum is	CC	
CC	an opportunistic pathogen of the human urogenital tract that is a	CC	
CC	significant cause of adverse pregnancy outcome, neonatal disease, and	CC	
CC	suppurative arthritis. As the infections are commonly asymptomatic, it is	CC	
CC	important to have specific and sensitive methods for detecting their	CC	
CC	presence in a patient. Also, as the pathogen has no current antibiotic	CC	
CC	directed specifically against it, it would be advantageous to isolate and	CC	
CC	detect gene sequences which are unique to it, and utilise these as a	CC	
CC	basis for diagnosis of U. urealyticum infection as well as to develop new	CC	
CC	and improved drug therapies. The present invention provides such novel	CC	
CC	polynucleotide sequences (AAX9501-681).	CC	
SQ	Sequence 1887 BP; 770 A; 210 C; 228 G; 679 T; 0 other;	XX	
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Db	473 TGAATTCCTGGATTAATTAACCATCTAGCAAAATTCTTGCGGAATTATAA 414	XX	
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Best Local Similarity	49.5%; Pred. No. 2.4;	XX	
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Mon Jun 17 12:37:28 2002

us-09-647-522-4.rng

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Searched:	383533 seqs, 12816752 residues			
Total number of hits satisfying chosen parameters:	767066			
Minimum DB seq length:	0			
Maximum DB seq length:	200000000			
Post-processing:	Minimum Match 0%			
	Maximum Match 100%			
	Listing first 45 summaries			
Database :	Issued_Patents_NA:*			
	1: /cgn2_6/podata/2/ina/5A_COMB.seq:*			
	2: /cgn2_6/podata/2/ina/5B_COMB.seq:*			
	3: /cgn2_6/podata/2/ina/6A_COMB.seq:*			
	4: /cgn2_6/podata/2/ina/6B_COMB.seq:*			
	5: /cgn2_6/podata/2/ina/PCTUS_COMB.seq:*			
	6: /cgn2_6/podata/2/ina/backfilesl.seq:*			
Pred. No.	1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Score	Query Match Length	DB ID	Description
C 1	48.6	3.0	7218	1 US-08-332-463-14/C Sequence 14, Appl
C 2	36.8	2.3	518	1 US-08-384-A-2 Sequence 2, Appl
C 3	35	2.2	289	4 US-09-007-005-17 Sequence 17, Appl
C 4	35	2.2	289	4 US-09-044-956-17 Sequence 17, Appl
C 5	34.8	2.2	4165	1 US-08-095-737-1 Sequence 1, Appl
C 6	34.8	2.2	4165	1 US-08-480-45-1 Sequence 1, Appl
C 7	34.8	2.2	4165	2 US-08-477-389-1 Sequence 1, Appl
C 8	34	2.1	778	3 US-09-188-930-27 Sequence 27, Appl
C 9	34	2.1	778	3 US-09-188-930-202 Sequence 202, Appl
C 10	34	2.1	5352450-1	Patent No. 5352450
C 11	34	2.1	43795	3 US-08-442-185-101 Sequence 101, Appl
C 12	33.4	2.1	1419	1 US-08-242-098-39 Sequence 39, Appl
C 13	33.2	2.1	885	4 US-08-952-009A-2, Sequence 2, Appl
C 14	33.2	2.1	1588	4 US-08-952-089A-26 Sequence 26, Appl
C 15	33.2	2.1	4146	4 US-08-952-089A-29 Sequence 29, Appl
C 16	32.5	2.0	1857	4 US-09-299-378-3 Sequence 3, Appl
C 17	32.6	2.0	48974	4 US-08-422-17 Sequence 17, Appl
C 18	32.4	2.0	1115	1 US-08-784-651-9 Sequence 9, Appl
C 19	32.4	2.0	4865	3 US-08-694-017-24 Sequence 24, Appl
C 20	32.2	2.0	943	4 US-08-936-165A-4 Sequence 34, Appl
C 21	31.8	2.0	3283	4 US-09-061-709-8 Sequence 8, Appl
C 22	31.8	2.0	3412	4 US-09-061-709-6 Sequence 6, Appl
C 23	31.6	2.0	332	4 US-09-439-313-207 Sequence 207, Appl
C 24	31.6	2.0	277	4 US-09-007-005-3 Sequence 3, Appl
C 25	31.4	2.0	277	4 US-09-244-709-3 Sequence 41, Appl
C 26	31.4	2.0	377	3 US-08-946-026-41 Sequence 41, Appl

ALIGNMENTS

RESULT	1	US-08-232-463-14/C
SEQUENCE	No.	Application US/08232463
PATENT NO.	5670367	
GENERAL INFORMATION:		
APPLICANT:	DORNER, F.	
APPLICANT:	SCHIEFLINGER, F.	
TITLE OF INVENTION:	RECOMBINANT FOWLPox VIL	
NUMBER OF SEQUENCES:	52	
CORRESPONDENCE ADDRESS:		
ADRESSEE:	Foley & Lardner	
STREET:	1800 Diagonal Road, Suite 500	
CITY:	Alexandria	
STATE:	VA	
COUNTRY:	USA	
ZIP:	22313-0299	
COMPUTER READABLE FORM:		
OPERATING SYSTEM:	PC-DOS/MS-DOS	
SOFTWARE:	Patent Release #1.0, Version	
CURRENT APPLICATION DATA:		
APPLICATION NUMBER:	US/08/232,463	
FILED DATE:		
CLASSIFICATION:	435	
PRIOR APPLICATION DATA:		
APPLICATION NUMBER:	US/07/935,313	
FILED DATE:		
APPLICATION NUMBER:	EP 91 114 300.6	
FILING DATE:	26-AUG-1991	
ATTORNEY/AGENT INFORMATION:		
NAME:	BENT, Stephen A.	
REGISTRATION NUMBER:	29,758	
REFERENCE/DOCKET NUMBER:	30472/114 IMMU	
TELECOMMUNICATION INFORMATION:		
TELEPHONE:	(703) 836-9300	
TELEFAX:	(703) 683-4109	
TELEX:	899149	
INFORMATION FOR SEQ ID NO:	14:	
SEQUENCE CHARACTERISTICS:		
LENGTH:	7218 basepairs	
TYPE:	nucleic acid	
STRANDEDNESS:	single	
TOPOLOGY:	linear	
IMMEDIATE SOURCE:		
CLONE:	PTZgpt-F1s	
US-08-232-463-14		

Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 243, Appli  
Sequence 25, Appli  
Sequence 24, Appli  
Sequence 24, Appli  
Sequence 24, Appli  
Sequence 24, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 335, Appli  
Sequence 16, Appli  
Patient No. 5240106  
Sequence 13, Appli











**RESULT** 14  
 US-08-952-089A-26  
 Sequence 26, Application US/08952089A  
 Patent No. 6165749  
**GENERAL INFORMATION:**  
 APPLICANT: SAGAWA, HIROAKI  
 APPLICANT: UENO, HARUMI  
 APPLICANT: OSHIMA, ATSUSHI  
 APPLICANT: KATO, IKINOSHIN  
 NUMBER OF SEQUENCES: 33  
**CORRESPONDENCE ADDRESS:**  
 ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP  
 STREET: PO BOX 747  
 CITY: FALLS CHURCH  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22040-0747  
**COMPUTER READABLE FORM:**  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
**CURRENT APPLICATION DATA:**  
 APPLICATION NUMBER: US/08/952,089A  
 FILING DATE:  
 CLASSIFICATION: 435  
**ATTORNEY/AGENT INFORMATION:**  
 NAME: WEINER, MARC S.  
 REGISTRATION NUMBER: 32,181  
 REFERENCE/DOCKET NUMBER: 1422-0319P  
**TELECOMMUNICATION INFORMATION:**  
 TELEPHONE: 703-205-8000  
 TELEFAX: 703-205-8050  
**INFORMATION FOR SEQ ID NO: 26:**  
**SEQUENCE CHARACTERISTICS:**  
 LENGTH: 1588 base pairs  
 STRANDEDNESS: double  
 TYPE: nucleic acid  
 TOPOLOGY: linear  
**MOLECULE TYPE:** DNA (genomic)  
 ; US-08-952-089A-26  
  

Query Match 2.1%; Score 33.2; DB 4; Length 1588;  
 Best Local Similarity 45.9%; Pred. No. 3.3;  
 Matches 113; Conservative 0; Mismatches 133; Indels 0; Gaps 0;  
 QY 420 agccaagaactcggtgcgcgttattgtataagcgtttaaagcaagatccggatggc 479  
 Db 1942 AGCRAAGATTCAATTACTGATTTTGAAATTACAATAAGTGTTCAGATTTRCC 2001  
 QY 587 AGCAGAAGATTCAATTACTGATTTTGAAATTACAATAAGTGTTCAGATTTRCC 646  
 Db 480 catccaaagacatcgaggatggccaaagagatgttcgtatcatcgccatccatca 539  
 QY 647 CAMGTGAACTAACATACATAGTCAAAGGGATTTATATCCATCAATATGC 706  
 Db 2062 TGGAAACATAAAATCCCTAACAACTCAATAGAAAGTTTATTCAGAAAAAAAGT 2121  
 QY 540 ggcatggaaacacgaggatcgccatcttacagatgcggccatggatcatcgccatgt 599  
 Db 707 TGGAAACATAAAATTCAGTAAAGCAATCAATAGAAGTTTATTCAGGAAAAGT 766  
 QY 600 tcctgtttatataattttagtaattttccggaaatgttgagacgacatccaaaggcg 659  
 Db 2122 TTTCATGATTAATTCAGTAAACTGATATAGTTTGAATAATAGGAAACAAAAAC 2181  
 QY 660 aacaaac 665  
 Db 2182 TGTAAAC 2187

Query Match 2.1%; Score 33.2; DB 4; Length 4146;  
 Best Local Similarity 45.9%; Pred. No. 5.8;  
 Matches 113; Conservative 0; Mismatches 133; Indels 0; Gaps 0;  
 QY 420 agccaagaactcggtgcgcgttattgtataagcgtttaaagcaagatccggatggc 479  
 Db 1942 AGCRAAGATTCAATTACTGATTTTGAAATTACAATAAGTGTTCAGATTTRCC 2001  
 QY 480 catccaaagacatcgaggatggccaaagagatgttcgtatcatcgccatccatca 539  
 Db 2002 CAATGTAACTCAATAATACAGTGTAAAGGAGGATTTAATATCCATCAATATGC 2061  
 QY 540 ggcatggaaacacgaggatcgccatggatcatcgccatgttcgtatccaaaggcg 599  
 Db 2062 TGGAAACATAAAATCCCTAACAACTCAATAGAAAGTTTATTCAGAAAAAAAGT 2121  
 QY 600 tcctgtttatataattttagtaattttccggaaatgttgagacgacatccaaaggcg 659  
 Db 2122 TTTCATGATTAATTCAGTAAACTGATATAGTTTGAATAATAGGAAACAAAAAC 2181

Mon Jun 17 12:37:29 2002

us-09-647-522-4.rni



RESULT 2		RESULT 3	
CNS04E5M/C	CNS039G/C	CNS04E5M	CNS039G
LOCUS	LOCUS	LOCUS	LOCUS
DEFINITION	DEFINITION	DEFINITION	DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone 103P02 of library G from Tetraodon nigroviridis, genomic survey sequence.	Drosophila melanogaster genome survey sequence Tm3 end of BAC # BAC0Bk10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.		
ACCESSION	ACCESSION	VERSION	VERSION
AL286627	AL063921	AL063921.1	AL063921.1
VERSTION	VERSTION	GI	GI
QY	QY	1424	1424
KEYWORDS	KEYWORDS	acatcaacacgtcggacttaatccatataatggaaatcgccaaaggcatacaatataagcat	atggagtatcacataatggaaatcgccaaaggcatacaatataagcat
GSS; genome survey sequence.		1427	1427
SOURCE	SOURCE		
ORGANISM	ORGANISM		
Tetraodon nigroviridis	Drosophila melanogaster		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleosteii; Neoteleosteii; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon nigroviridis.	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidea; Drosophilidae; Drosophila.		
REFERENCE	REFERENCE		
AUTHORS	AUTHORS		
Roest-Crollius,H., Jaijou,O., Basilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.	Direct Submission		
JOURNAL	JOURNAL		
CHARACTERIZATION AND REPEAT ANALYSIS OF THE COMPACT GENOME OF THE FRESHWATER PUFFERFISH TETRAODON NIGROVIRIDIS	Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage : BP 191 91006 EVRY CEDEX - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
REFERENCE	COMMENT		
AUTHORS			
Roest-Crollius,H., Jaijou,O., Basilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <a href="http://www.fruitfly.org">http://www.fruitfly.org</a> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Hammeser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; on bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BAC/PAC Resource Center can be found at <a href="http://bacpac.med.buffalo.edu/drosophila_bac.htm">http://bacpac.med.buffalo.edu/drosophila_bac.htm</a> .		
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